

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/921,060DATE: 10/09/98  
TIME: 14:03:44

INPUT SET: S29040.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

ENTERED

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: ANDERSON, Darrell R.  
HANNA, Nabil  
LEONARD, John E.  
NEWMAN, Roland A.  
REFF, Mitchell E.  
RASTETTER, William H.

(ii) TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND  
RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED  
DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL  
LYMPHOMA

(iii) NUMBER OF SEQUENCES: 11

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
(B) STREET: P.O. Box 1404  
(C) CITY: Alexandria  
(D) STATE: Virginia  
(E) COUNTRY: United States  
(F) ZIP: 22313-1404

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/921,060  
(B) FILING DATE: 29-AUG-1997  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/149,099  
(B) FILING DATE: 03-NOV-1993

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/978,891  
(B) FILING DATE: 13-NOV-1992

## (viii) ATTORNEY/AGENT INFORMATION:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/921,060DATE: 10/09/98  
TIME: 14:03:46

INPUT SET: S29040.raw

47 (A) NAME: Teskin, Robin L.  
48 (B) REGISTRATION NUMBER: 35,030  
49 (C) REFERENCE/DOCKET NUMBER: 012712-432  
50

51 (ix) TELECOMMUNICATION INFORMATION:  
52 (A) TELEPHONE: (703) 836-6620  
53 (B) TELEFAX: (703) 836-2021  
54  
55

56 (2) INFORMATION FOR SEQ ID NO:1:  
57

58 (i) SEQUENCE CHARACTERISTICS:  
59 (A) LENGTH: 27 base pairs  
60 (B) TYPE: nucleic acid  
61 (C) STRANDEDNESS: single  
62 (D) TOPOLOGY: linear  
63

64 (ii) MOLECULE TYPE: DNA (genomic)  
65  
66  
67

68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
69  
70

71 GGGAGCTTGG ATCGATCCTC TATGGTT  
72

27

73 (2) INFORMATION FOR SEQ ID NO:2:  
74

75 (i) SEQUENCE CHARACTERISTICS:  
76 (A) LENGTH: 8540 base pairs  
77 (B) TYPE: nucleic acid  
78 (C) STRANDEDNESS: single  
79 (D) TOPOLOGY: circular  
80

81 (ii) MOLECULE TYPE: DNA (genomic)  
82

83 (iii) HYPOTHETICAL: NO  
84

85 (iv) ANTI-SENSE: NO  
86  
87  
88  
89

90 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
91

92	GACGTCGCGG CCGCTCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG	60
93		
94	AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC	120
95		
96	GGAGAATGGG CGGAACTGGG CGGAGTTAGG GCGGGGATGG GCGGAGTTAG GGGCGGGACT	180
97		
98	ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG	240
99		

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103		
104	AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC	420
105		
106	GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG	480
107		
108	ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA	540
109		
110	TGGGTGGACT ATTTACGGTA AACTGCCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA	600
111		
112	AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATTG TGGCCAGTAC	660
113		
114	ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC	720
115		
116	ATGGTGATGC GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA	780
117		
118	TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG	840
119		
120	GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA	900
121		
122	CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC	960
123		
124	CATCACAGAT CTCTCACCAT GAGGGTCCCC GCTCAGCTCC TGGGGCTCCT GCTGCTCTGG	1020
125		
126	CTCCAGGTG CACGATGTGA TGGTACCAAG GTGGAATCA AACGTACGGT GGCTGCACCA	1080
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128	TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAAGTGC CTCTGTTGTG	1140
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130	TGCCTGCTGA ATAACTTCTA TCCCAGAGAG GCCAAAGTAC AGTGGAAGGT GGATAACGCC	1200
131		
132	CTCCAATCGG GTAACCTCCA GGAGAGTGTC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC	1260
133		
134	AGCCTCAGCA GCACCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC	1320
135		
136	TGCGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG	1380
137		
138	TGTTGAATTC AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCTG GACAACATGC	1440
139		
140	GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT	1500
141		
142	GTTTGGCCCT CCCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCCAC TGTCCCTTCC	1560
143		
144	TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT	1620
145		
146	GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGAAGACA ATAGCAGGCA TGCTGGGGAT	1680
147		
148	GCGGTGGGCT CTATGGAACC AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG	1740
149		
150	ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT	1800
151		
152	TTCTACTTGC GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT	1860

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153	GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC	1920
154		
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156		
157	GTAACAACTC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA	2040
158		
159	TAAGCAGAGC TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCGAC	2100
160		
161	ATGGGTTGGA GCCTCATCTT GCTCTTCCTT GTCGCTGTTG CTACGCGTGT CGCTAGCACC	2160
162		
163	AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG	2220
164		
165	GCCCTGGGCT GCCTGGTCAA GGACTIONC CCCGAACCGG TGACGGTGTC GTGGAACCTCA	2280
166		
167	GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC	2340
168		
169	TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC	2400
170		
171	AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGCAGAGCC CAAATCTTGT	2460
172		
173	GACAAAACCTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC	2520
174		
175	TTCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA	2580
176		
177	TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC	2640
178		
179	GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC	2700
180		
181	CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGACTIONAAG	2760
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183	TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA	2820
184		
185	GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAGG	2880
186		
187	AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG	2940
188		
189	TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC	3000
190		
191	GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG	3060
192		
193	AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC	3120
194		
195	CTCTCCCTGT CTCCGGGTAA ATGAGGATCC GTTAACGGTT ACCAACTACC TAGACTGGAT	3180
196		
197	TCGTGACAAC ATGCGGCCGT GATATCTACG TATGATCAGC CTCGACTGTG CCTTCTAGTT	3240
198		
199	GCCAGCCATC TGTTGTTTGC CCCTCCCCCG TGCTTCTCTT GACCCTGGAA GGTGCCACTC	3300
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201	CCACTGTCCT TTCCTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGTCATT	3360
202		
203	CTATTCTGGG GGGTGGGGTG GGGCAGGACA GCAAGGGGA GGATTGGGAA GACAATAGCA	3420
204		
205		

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206	GGCATGCTGG	GGATGCGGTG	GGCTCTATGG	AACCAGCTGG	GGCTCGACAG	CGCTGGATCT	3480
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208	CCCGATCCCC	AGCTTTGCTT	CTCAATTTCT	TATTTGCATA	ATGAGAAAAA	AAGGAAAATT	3540
209							
210	AATTTTAACA	CCAATTCAGT	AGTTGATTGA	GCAAATGCGT	TGCCAAAAAG	GATGCTTTAG	3600
211							
212	AGACAGTGTT	CTCTGCACAG	ATAAGGACAA	ACATTATTCA	GAGGGAGTAC	CCAGAGCTGA	3660
213							
214	GACTCCTAAG	CCAGTGAGTG	GCACAGCATT	CTAGGGAGAA	ATATGCTTGT	CATCACCGAA	3720
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216	GCCTGATTCC	GTAGAGCCAC	ACCTTGGTAA	GGGCCAATCT	GCTCACACAG	GATAGAGAGG	3780
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218	GCAGGAGCCA	GGGCAGAGCA	TATAAGGTGA	GGTAGGATCA	GTTGCTCCTC	ACATTTGCTT	3840
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220	CTGACATAGT	TGTGTTGGGA	GCTTGGATAG	CTTGGACAGC	TCAGGGCTGC	GATTTGCGGC	3900
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222	CAAACTTGAC	GGCAATCCTA	GCGTGAAGGC	TGGTAGGATT	TTATCCCCGC	TGCCATCATG	3960
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224	GTTTCGACCAT	TGAACTGCAT	CGTCGCCGTG	TCCCAAAATA	TGGGGATTGG	CAAGAACGGA	4020
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226	GACCTACCCCT	GGCCTCCGCT	CAGGAACGAG	TTCAAGTACT	TCCAAAGAAT	GACCACAACC	4080
227							
228	TCTTCAGTGG	AAGGTAAACA	GAATCTGGTG	ATTATGGGTA	GGAAAACCTG	GTTCTCCATT	4140
229							
230	CCTGAGAACA	ATCGACCTTT	AAAGGACAGA	ATTAATATAG	TTCTCAGTAG	AGAACTCAAA	4200
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232	GAACCACCAC	GAGGAGCTCA	TTTTCTTGCC	AAAAGTTTGG	ATGATGCCTT	AAGACTTATT	4260
233							
234	GAACAACCGG	AATTGGCAAG	TAAAGTAGAC	ATGGTTTGGG	TAGTCGGAGG	CAGTTCTGTT	4320
235							
236	TACCAGGAAG	CCATGAATCA	ACCAGGCCAC	CTTAGACTCT	TTGTGACAAG	GATCATGCAG	4380
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240	GAATACCCAG	GCGTCCTCTC	TGAGGTCCAG	GAGGAAAAAG	GCATCAAGTA	TAAGTTTGAA	4500
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242	GTCTACGAGA	AGAAAGACTA	ACAGGAAGAT	GCTTTCAAGT	TCTCTGCTCC	CCTCCTAAAG	4560
243							
244	TCATGCATTT	TTATAAGACC	ATGGGACTTT	TGCTGGCTTT	AGATCAGCCT	CGACTGTGCC	4620
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247							
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251							
252	CAATAGCAGG	CATGCTGGGG	ATGCGGTGGG	CTCTATGGAA	CCAGCTGGGG	CTCGAGCTAC	4860
253							
254	TAGCTTTGCT	TCTCAATTTT	TTATTTGCAT	AATGAGAAAA	AAAGGAAAAA	TAATTTTAAC	4920
255							
256	ACCAATTCAG	TAGTTGATTG	AGCAAATGCG	TTGCCAAAAA	GGATGCTTTA	GAGACAGTGT	4980
257							
258	TCTCTGCACA	GATAAGGACA	AACATTATTC	AGAGGGAGTA	CCCAGAGCTG	AGACTCCTAA	5040

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**SEQUENCE VERIFICATION REPORT**  
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